

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Lal, Preeti  
Guegler, Karl J.  
Corley, Neil C.

(ii) TITLE OF INVENTION: PROSTATE GROWTH-ASSOCIATED MEMBRANE PROTEINS

(iii) NUMBER OF SEQUENCES: 7

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
(B) STREET: 3174 PORTER DRIVE  
(C) CITY: PALO ALTO  
(D) STATE: CALIFORNIA  
(E) COUNTRY: USA  
(F) ZIP: 94304

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: To Be Assigned  
(B) FILING DATE: Herewith  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: CERRONE, MICHAEL C.  
(B) REGISTRATION NUMBER: 39,132  
(C) REFERENCE/DOCKET NUMBER: PF-0527 US

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (650) 855-0555  
(B) TELEFAX: (650) 845-4166

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 141 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: PROSTUT10  
(B) CLONE: 1691243

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1 :

Met Val His Val Ala Tyr Ser Leu Cys Leu Pro Met Arg Arg Ser  
 5 10 15  
 Glu Arg Tyr Leu Phe Leu Asn Met Ala Tyr Gln Gln Val His Ala  
 20 25 30  
 Asn Ile Glu Asn Ser Trp Asn Glu Glu Glu Val Trp Arg Ile Glu  
 35 40 45  
 Met Tyr Ile Ser Phe Gly Ile Met Ser Leu Gly Leu Leu Ser Leu  
 50 55 60  
 Leu Ala Val Thr Ser Ile Pro Ser Val Ser Asn Ala Leu Asn Trp  
 65 70 75  
 Arg Glu Phe Ser Phe Ile Gln Ser Thr Leu Gly Tyr Val Ala Leu  
 80 85 90  
 Leu Ile Ser Thr Phe His Val Leu Ile Tyr Gly Trp Lys Arg Ala  
 95 100 105  
 Phe Glu Glu Glu Tyr Tyr Arg Phe Tyr Thr Pro Pro Asn Phe Val  
 110 115 120  
 Leu Ala Leu Val Leu Pro Ser Ile Val Ile Leu Asp Leu Leu Gln  
 125 130 135  
 Leu Cys Arg Tyr Pro Asp  
 140

## (2) INFORMATION FOR SEQ ID NO: 2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 410 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRSTTUT03
- (B) CLONE: 1999442

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2 :

Met Phe Leu Pro Pro Val Val Leu Ala Ile Arg Ser Arg Tyr Val  
 5 10 15  
 Leu Glu Ala Ala Val Tyr Thr Phe Thr Met Phe Phe Ser Thr Phe  
 20 25 30  
 Tyr His Ala Cys Asp Gln Pro Gly Ile Val Val Phe Cys Ile Met  
 35 40 45  
 Asp Tyr Asp Val Leu Gln Phe Cys Asp Phe Leu Gly Ser Leu Met  
 50 55 60  
 Ser Val Trp Val Thr Val Ile Ala Met Ala Arg Leu Gln Pro Val  
 65 70 75  
 Val Lys Gln Val Leu Tyr Leu Leu Gly Ala Met Leu Leu Ser Met  
 80 85 90  
 Ala Leu Gln Leu Asp Arg His Gly Leu Trp Asn Leu Leu Gly Pro  
 95 100 105  
 Ser Leu Phe Ala Leu Gly Ile Leu Ala Thr Ala Trp Thr Val Arg  
 110 115 120  
 Ser Val Arg Arg Arg His Cys Tyr Pro Pro Thr Trp Arg Arg Trp  
 125 130 135  
 Leu Phe Tyr Leu Cys Pro Gly Ser Leu Ile Ala Gly Ser Ala Val  
 140 145 150  
 Leu Leu Tyr Ala Phe Val Glu Thr Arg Asn Tyr Phe Tyr Ile

155	160	165
His Ser Ile Trp His Met Leu Ile Ala Gly Ser Val Gly Phe Leu		
170	175	180
Leu Pro Pro Arg Ala Lys Thr Asp His Gly Val Pro Ser Gly Ala		
185	190	195
Arg Ala Arg Gly Cys Gly Tyr Gln Leu Cys Ile Asn Glu Gln Glu		
200	205	210
Glu Pro Gly Pro Arg Gly Pro Arg Arg Gly His Cys Gln Gln His		
215	220	225
Leu Cys Gln Leu Arg Gly Ala Leu Gly Leu Ala Leu Arg Gly Tyr		
230	235	240
Glu Cys Phe Leu Glu Phe Phe Leu Gly Val Trp Ser Pro Leu Arg		
245	250	255
Arg Arg Gln Ala Val Phe Leu Glu Asp Met Glu Ser Phe Ser Arg		
260	265	270
Thr Gln Asn Ser Ser Arg Asp Leu Glu Pro Phe Pro Gly His Gly		
275	280	285
Glu Leu Pro Glu Gly Leu Glu Ser Pro Cys Ile Met Glu Ser Phe		
290	295	300
Leu Arg Thr Gly Ala Tyr Ala Gly Thr Glu Ser Leu Arg Thr Lys		
305	310	315
Glu Ser Leu Leu Gln Val Trp Ser Leu Ser Trp Asp Ala Glu Pro		
320	325	330
Ser Gln Asp Met Asp Ser Phe Pro Gly Arg Gln Ser Pro Val Arg		
335	340	345
Ser Thr Ala Ser Phe Gln Arg Arg Trp Ser Leu Ser Trp Gly Asn		
350	355	360
Gln Ile Ser Arg Phe Ser Gln Arg Leu Ser Asn Ser Gly Leu Arg		
365	370	375
Leu Pro Ser Gln Arg Gln Arg Leu Gly Cys Ala Val Leu Trp Arg		
380	385	390
Arg Asp Cys Arg Met Asp Gly Ala Gly Thr Gly Ala Val Trp Val		
395	400	405
Ala Gly Ile Leu Val		
410		

## (2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PROSTUT10
- (B) CLONE: 1691243

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3 :

CAAGTATAGG AGATTTCCAC CTTGGTTGGA AACCTGGTTA CAGTGTAGAA AACAGCTTGG 60  
ATTACTAAGT TTTTTCTTCG CTATGGTCCA TGGTGCCTAC AGCCTCTGCT TACCGATGAG 120  
AAGGTCAAGAG AGATATTTGT TTCTCAACAT GGCTTATCAG CAGGTCATG CAAATATTGA 180  
AAACTCTTGG AATGAGGAAG AAGTTGGAG AATTGAAATG TATATCTCCT TTGGCATAAT 240  
GAGCCTTGGC TTACTTTCCC TCCTGGCAGT CACTTCTATC CCTTCAGTGA GCAATGCTTT 300  
AAACTGGAGA GAATTCAGTT TTATTCAGTC TACACTTGGA TATGTCGCTC TGCTCATAAG 360  
TACTTTCCAT GTTTAATTT ATGGATGGAA ACGAGCTTT GAGGAAGAGT ACTACAGATT 420  
TTATACACCA CCAAACTTG TTCTTGCTCT TGTTTGCCC TCAATTGTAA TTCTGGATCT 480

TTTGCAGCTT	TGCAGATACC	CAGACTGAGC	TGGAACCTGGA	ATTTGTCTTC	CTATTGACTC	540
TACTTCTTTA	AAAGCGGCTG	CCCATTACAT	TCCTCAGCTG	TCCTTCAGT	TAGGTGTACA	600
TGTGACTGAG	TGTTGGCCAG	TGAGATGAAG	TCTCCTCAAA	GGAAAGGCAGC	ATGTGTCTT	660
TTTCATCCCT	TCATCTTGCT	GCTGGGATTG	TGGATATAAC	AGGAGCCCTG	GCAGCTGTCT	720
CCAGAGGATC	AAAGCCACAC	CCAAAGAGTA	AGGCAGATA	GAGACCAGAA	AGACCTTGAC	780
TACTTCCCTA	CTTCCACTGC	TTTTCTCTGC	ATTTAAGCCA	TTGTAATCT	GGGTGTGTTA	840
CATGAAGTGA	AAATTAATTG	TTTCTGCCCT	TCAGTTCTT	ATCCTGATAC	CATTTAACAC	900
TGTCTGAATT	AACTAGACTG	CAATAATTCT	TTCTTTGAA	AGCTTTAAA	GGATAATGTG	960
CAATTACACAT	AAAAATTGAT	TTTCCATTGT	CAATTAGTTA	TACTCATT	CCTGCCTTGA	1020
TCTTTCATTA	GATATTTGT	ATCTGCTTGG	AATATATTAT	CTTCTTTTA	ACTGTGTAAT	1080
TGGTAATTAC	AAAAACTCTG	TAATCTCCAA	AATATTGCTA	TCAAATTACA	CACCATGTT	1140
TCTATCATTC	TCATAGATCT	GCCTTATAAA	CATTAAATAA	AAAAGTACTA	TTAATGATT	1200
						1213

## (2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1297 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRSTTUT03
- (B) CLONE: 1999442

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4 :

CGGACGCGTG	GGCTGCTCTG	CCTGAGCAAC	CTCATGTTTC	TGCCACCTGT	GGTCCTGGCC	60
ATTCGGAGTC	GATATGTGCT	GGAAAGCTGCA	GTCTACACCT	TCACCATGTT	CTTCTCCACG	120
TTCTATCATG	CCTGTGACCA	GCCAGGCATC	GTGGTTTCT	GCATCATGGA	CTACGATGTG	180
CTGCACTTCT	GTGATTTCT	GGGCTCTTA	ATGTCCGTGT	GGGTCACTGT	CATTGCCATG	240
GCTCGTTAC	AGCCCGTGGT	CAAGCAGGTG	CTGTATTTGC	TGGGAGCTAT	GCTGCTGTCC	300
ATGGCTCTGC	AGCTTGACCG	ACATGGACTC	TGGAACCTGC	TTGGACCCAG	TCTCTTCGCC	360
CTGGGGATCT	TGGGACACAGC	CTGGACAGTA	CGCAGCGTCC	GCCGCCGGCA	CTGCTACCCA	420
CCCACGTGGC	GCCGCTGGCT	TTTCTACTTG	TGCCCTGGCA	GCCTTATTGC	AGGCAGTGCC	480
GTCCTGCTT	ATGCTTTGT	GGAGACCCGG	GACAACTA	TCTACATTCA	CAGCATTGG	540
CATATGCTCA	TTGCGGGCAG	TGTGGCTTC	CTGCTGCC	CTCGTGC	GA	600
GGGGTCCCCAT	CTGGAGCCCG	GGCCCGGGC	TGTGGTTACC	AGCTATGCAT	CAACGAGCAG	660
GAGGAGCCTG	GGCCTCGTGG	GCCCAGGAGG	GGCCACTGTC	AGCAGCATCT	GTGCCAGCTG	720
AGAGGGGCTT	TGGGCTGGC	CCTGAGGGGA	TATGAATGCT	TCCTAGAGTT	CTTTCTGGG	780
GTGTGGAGCC	CTCTTAGAAG	GAGACAGGCT	GTATTTCTTG	AGGACATGGA	GTCTTCTCA	840
AGGACACAAA	ACTCTTCCAG	GGACCTGGAG	CCCTTCCCAG	GACATGGAGA	ACTTCCTGAG	900
GGCCTGGAGT	CCCCCTGCAT	CATGGAGTCC	TTCTTAAGGA	CTGGAGCCTA	TGCAGGCACA	960
GAGTCCCTCA	GGACCAAGGA	GTCCCTCCTG	CAGGTGTGGA	GCCTTCCTG	GGATGCAGAG	1020
CCTTCCCAAG	ACATGGATT	CTTCCCAGGG	AGACAAAGCC	CTGTCAGGAG	CACAGCATCT	1080
TCAGGAGGAA	GGTGGAGTCT	ATCTTGGGA	AACCAAATT	CCAGATTTTC	CCAGAGGCTC	1140
AGCAACTCTG	GCCTCAGGCT	TCCTTCCCAG	AGGCAGCGTC	TGGGCTGTGC	TGTGCTGTGG	1200
AGGAGGGATT	GCAGGATGGA	TGGAGCTGGG	ACTGGGGCTG	TCTGGGTGGC	TGGTATCCTC	1260
GTTTGATACA	GGTGGAGTCT	CTGTGCTCTC	ATAGAAG			1297

## (2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
(A) LIBRARY: GenBank  
(B) CLONE: 1216498

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5 :

Met Gly Arg Ala Met Val Val Arg Leu Gly Leu Gly Leu Leu Leu  
5 10 15  
Leu Ala Leu Leu Leu Pro Thr Gln Ile Tyr Cys Asn Gln Thr Ser  
20 25 30  
Val Ala Pro Phe Ser Gly Asn Gln Ser Ile Ser Ala Ala Pro Asn  
35 40 45  
Pro Thr Asn Ala Thr Thr Arg Ser Gly Cys Ser Ser Leu Gln Ser  
50 55 60  
Thr Ala Gly Leu Leu Ala Leu Ser Leu Ser Leu Leu His Leu Tyr  
65 70 75  
Cys

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 261 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
(A) LIBRARY: GenBank  
(B) CLONE: 130989

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6 :

Met Trp Val Pro Val Val Phe Leu Thr Leu Ser Val Thr Trp Ile  
5 10 15  
Gly Ala Ala Pro Leu Ile Leu Ser Arg Ile Val Gly Gly Trp Glu  
20 25 30  
Cys Glu Lys His Ser Gln Pro Trp Gln Val Leu Val Ala Ser Arg  
35 40 45  
Gly Arg Ala Val Cys Gly Gly Val Leu Val His Pro Gln Trp Val  
50 55 60  
Leu Thr Ala Ala His Cys Ile Arg Asn Lys Ser Val Ile Leu Leu  
65 70 75  
Gly Arg His Ser Leu Phe His Pro Glu Asp Thr Gly Gln Val Phe  
80 85 90  
Gln Val Ser His Ser Phe Pro His Pro Leu Tyr Asp Met Ser Leu  
95 100 105  
Leu Lys Asn Arg Phe Leu Arg Pro Gly Asp Asp Ser Ser His Asp  
110 115 120  
Leu Met Leu Leu Arg Leu Ser Glu Pro Ala Glu Leu Thr Asp Ala  
125 130 135  
Val Lys Val Met Asp Leu Pro Thr Gln Glu Pro Ala Leu Gly Thr  
140 145 150  
Thr Cys Tyr Ala Ser Gly Trp Gly Ser Ile Glu Pro Glu Glu Phe  
155 160 165  
Leu Thr Pro Lys Lys Leu Gln Cys Val Asp Leu His Val Ile Ser  
170 175 180  
Asn Asp Val Cys Ala Gln Val His Pro Gln Lys Val Thr Lys Phe  
185 190 195

Met	Leu	Cys	Ala	Gly	Arg	Trp	Thr	Gly	Gly	Lys	Ser	Thr	Cys	Ser
200								205						210
Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Asn	Gly	Val	Leu	Gln	Gly
215								220						225
Ile	Thr	Ser	Trp	Gly	Ser	Glu	Pro	Cys	Ala	Leu	Pro	Glu	Arg	Pro
230								235						240
Ser	Leu	Tyr	Thr	Lys	Val	Val	His	Tyr	Arg	Lys	Trp	Ile	Lys	Asp
245								250						255
Thr	Ile	Val	Ala	Asn	Pro									
260														

## (2) INFORMATION FOR SEQ ID NO: 7:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1317 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 2459993

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7 :

Met	Leu	Ala	Cys	Leu	Cys	Cys	Lys	Lys	Gly	Gly	Ile	Gly	Phe	Lys
5								10						15
Glu	Phe	Glu	Asn	Ala	Glu	Gly	Asp	Glu	Tyr	Val	Ala	Asp	Phe	Ser
20								25						30
Glu	Gln	Gly	Ser	Pro	Ala	Ala	Ala	Gln	Thr	Gly	Pro	Asp	Val	
35								40						45
Tyr	Val	Leu	Pro	Leu	Thr	Glu	Val	Ser	Leu	Pro	Met	Ala	Lys	Gln
50								55						60
Pro	Gly	Arg	Ser	Val	Gln	Leu	Leu	Lys	Ser	Thr	Asp	Leu	Gly	Arg
65								70						75
His	Ser	Leu	Leu	Tyr	Leu	Lys	Glu	Ile	Gly	His	Gly	Trp	Phe	Gly
80								85						90
Lys	Val	Phe	Leu	Gly	Glu	Val	His	Ser	Gly	Val	Ser	Gly	Thr	Gln
95								100						105
Val	Val	Val	Lys	Glu	Leu	Lys	Val	Ser	Ala	Ser	Val	Gln	Glu	Gln
110								115						120
Met	Gln	Phe	Leu	Glu	Glu	Ala	Gln	Pro	Tyr	Arg	Ala	Leu	Gln	His
125								130						135
Ser	Asn	Leu	Leu	Gln	Cys	Leu	Ala	Gln	Cys	Ala	Glu	Val	Thr	Pro
140								145						150
Tyr	Leu	Leu	Val	Met	Glu	Phe	Cys	Pro	Leu	Gly	Asp	Leu	Lys	Gly
155								160						165
Tyr	Leu	Arg	Ser	Cys	Arg	Val	Thr	Glu	Ser	Met	Ala	Pro	Asp	Pro
170								175						180
Leu	Thr	Leu	Gln	Arg	Met	Ala	Cys	Glu	Val	Ala	Cys	Gly	Val	Leu
185								190						195
His	Leu	His	Arg	His	Asn	Tyr	Val	His	Ser	Asp	Leu	Ala	Leu	Arg
200								205						210
Asn	Cys	Leu	Leu	Thr	Ala	Asp	Leu	Thr	Val	Lys	Val	Gly	Asp	Tyr
215								220						225
Gly	Leu	Ser	His	Cys	Lys	Tyr	Arg	Glu	Asp	Tyr	Leu	Val	Thr	Ala
230								235						240
Asp	Gln	Leu	Trp	Val	Pro	Leu	Arg	Trp	Ile	Ala	Pro	Glu	Leu	Val

245	Asp Glu Val His Gly Asn Leu Leu Val	250	Asp Gln Thr Lys Ser	255
260	265	265	270	
Ser Asn Val Trp Ser Leu Gly Val Thr	Ile Trp Glu Leu Phe	Glu	285	
275	280	280	285	
Leu Gly Ala Gln Pro Tyr Pro Gln His	Ser Asp Arg Gln Val	Leu	300	
290	295	295	300	
Ala Tyr Ala Val Arg Glu Gln Gln Leu	Lys Leu Pro Lys Pro	Gln	315	
305	310	310	315	
Leu Gln Leu Ala Leu Ser Asp Arg Trp	Tyr Glu Val Met Gln	Phe	330	
320	325	325	330	
Cys Trp Leu Gln Pro Glu Gln Arg Pro	Thr Ala Glu Glu Val	His	345	
335	340	340	345	
Leu Leu Leu Ser Tyr Leu Cys Ala Lys	Gly Thr Thr Glu Leu	Glu	360	
350	355	355	360	
Glu Glu Phe Glu Arg Arg Trp Arg Ser	Leu Arg Pro Gly Gly	Ser	375	
365	370	370	375	
Thr Gly Leu Gly Ser Gly Ser Ala Ala	Pro Ala Ala Ala Thr	Ala	390	
380	385	385	390	
Ala Ser Ala Glu Leu Thr Ala Ala Ser	Ser Phe Pro Leu Leu	Glu	405	
395	400	400	405	
Arg Phe Thr Ser Asp Gly Phe His Val	Asp Ser Asp Asp Val	Leu	420	
410	415	415	420	
Thr Val Thr Glu Thr Ser His Gly Leu	Asn Phe Glu Tyr Lys	Trp	435	
425	430	430	435	
Glu Ala Gly Cys Gly Ala Glu Glu Tyr	Pro Pro Ser Gly Ala	Ala	450	
440	445	445	450	
Ser Ser Pro Gly Ser Ala Ala Arg Leu	Gln Glu Leu Cys Ala	Pro	465	
455	460	460	465	
Asp Ser Ser Pro Pro Gly Val Val Pro	Val Leu Ser Ala His	Ser	480	
470	475	475	480	
Pro Ser Val Gly Ser Glu Tyr Phe Ile	Arg Leu Glu Gly Ala	Val	495	
485	490	490	495	
Pro Ala Ala Gly His Asp Pro Asp Cys	Ala Gly Cys Ala Pro	Ser	510	
500	505	505	510	
Pro Gln Ala Val Thr Asp Gln Asp Asn	Asn Ser Glu Glu Ser	Thr	525	
515	520	520	525	
Val Ala Ser Leu Ala Met Glu Pro Leu	Leu Gly His Ala Pro	Pro	540	
530	535	535	540	
Thr Glu Gly Leu Trp Gly Pro Cys Asp	His His Ser His Arg	Arg	555	
545	550	550	555	
Gln Gly Ser Pro Cys Pro Ser Arg Ser	Pro Ser Pro Gly Thr	Pro	570	
560	565	565	570	
Met Leu Pro Ala Glu Asp Ile Asp Trp	Gly Val Ala Thr Phe	Cys	585	
575	580	580	585	
Pro Pro Phe Phe Asp Asp Pro Leu Gly	Ala Ser Pro Ser Gly	Ser	600	
590	595	595	600	
Pro Gly Ala Gln Pro Ser Pro Ser Asp	Glu Glu Pro Glu Glu	Gly	615	
605	610	610	615	
Lys Val Gly Leu Ala Ala Gln Cys Gly	His Trp Ser Ser Asn	Met	630	
620	625	625	630	
Ser Ala Asn Asn Asn Ser Ala Ser Arg	Asp Pro Glu Ser Trp	Asp	645	
635	640	640	645	
Pro Gly Tyr Val Ser Ser Phe Thr Asp	Ser Tyr Arg Asp Asp	Cys	660	
650	655	655	660	
Ser Ser Leu Glu Gln Thr Pro Arg Ala	Ser Pro Glu Val Gly	His	675	
665	670	670	675	
Leu Leu Ser Gln Glu Asp Pro Arg Asp	Phe Leu Pro Gly Leu	Val	690	
680	685	685	690	
Ala Val Ser Pro Gly Gln Glu Pro Ser	Arg Pro Phe Asn Leu	Leu	705	
695	700	700	705	

Pro Leu Cys Pro Ala Lys Gly Leu Ala Pro Ala Ala Cys Leu Ile  
 710 715 720  
 Thr Ser Pro Trp Thr Glu Gly Ala Val Gly Gly Ala Glu Asn Pro  
 725 730 735  
 Ile Val Glu Pro Lys Leu Ala Gln Glu Ala Glu Gly Ser Ala Glu  
 740 745 750  
 Pro Gln Leu Pro Leu Pro Ser Val Pro Ser Pro Ser Cys Glu Gly  
 755 760 765  
 Ala Ser Leu Pro Ser Glu Glu Ala Ser Ala Pro Asp Ile Leu Pro  
 770 775 780  
 Ala Ser Pro Thr Pro Ala Ala Gly Ser Trp Val Thr Val Pro Glu  
 785 790 795  
 Pro Ala Pro Thr Leu Glu Ser Ser Gly Ser Ser Leu Gly Gln Glu  
 800 805 810  
 Ala Pro Ser Ser Glu Asp Glu Asp Thr Thr Glu Ala Thr Ser Gly  
 815 820 825  
 Val Phe Thr Asp Leu Ser Ser Asp Gly Pro His Thr Glu Lys Ser  
 830 835 840  
 Gly Ile Val Pro Ala Leu Arg Ser Leu Gln Lys Gln Val Gly Thr  
 845 850 855  
 Pro Asp Ser Leu Asp Ser Leu Asp Ile Pro Ser Ser Ala Ser Asp  
 860 865 870  
 Gly Gly Cys Glu Val Leu Ser Pro Ser Ala Ala Gly Pro Pro Gly  
 875 880 885  
 Gly Gln Pro Arg Ala Val Asp Ser Gly Tyr Asp Thr Glu Asn Tyr  
 890 895 900  
 Glu Ser Pro Glu Phe Val Leu Lys Glu Ala His Glu Ser Ser Glu  
 905 910 915  
 Pro Glu Ala Phe Gly Glu Pro Ala Ser Glu Gly Glu Ser Pro Gly  
 920 925 930  
 Pro Asp Pro Leu Leu Ser Val Ser Leu Gly Gly Leu Ser Lys Lys  
 935 940 945  
 Ser Pro Tyr Arg Asp Ser Ala Tyr Phe Ser Asp Leu Asp Ala Glu  
 950 955 960  
 Ser Glu Pro Thr Phe Gly Pro Glu Lys His Ser Gly Ile Gln Asp  
 965 970 975  
 Ser Gln Lys Glu Gln Asp Leu Arg Ser Pro Pro Ser Pro Gly His  
 980 985 990  
 Gln Ser Val Gln Ala Phe Pro Arg Ser Ala Val Ser Ser Glu Val  
 995 1000 1005  
 Leu Ser Pro Pro Gln Gln Ser Glu Glu Pro Leu Pro Glu Val Pro  
 1010 1015 1020  
 Arg Pro Glu Pro Leu Gly Ala Gln Gly Pro Val Gly Val Gln Pro  
 1025 1030 1035  
 Val Pro Gly Pro Ser His Ser Lys Cys Phe Pro Leu Thr Ser Val  
 1040 1045 1050  
 Pro Leu Ile Ser Glu Gly Ser Gly Thr Glu Pro Gln Gly Pro Ser  
 1055 1060 1065  
 Gly Gln Leu Ser Gly Arg Ala Gln Gln Gly Gln Met Gly Asn Pro  
 1070 1075 1080  
 Ser Thr Pro Arg Ser Pro Leu Cys Leu Ala Leu Pro Gly His Pro  
 1085 1090 1095  
 Gly Ala Leu Glu Gly Arg Pro Glu Glu Asp Glu Asp Thr Glu Asp  
 1100 1105 1110  
 Ser Glu Glu Ser Asp Glu Glu Leu Arg Cys Tyr Ser Val Gln Glu  
 1115 1120 1125  
 Pro Ser Glu Asp Ser Glu Glu Glu Pro Pro Ala Val Pro Val Val  
 1130 1135 1140  
 Val Ala Glu Ser Gln Ser Ala Arg Asn Leu Arg Ser Leu Leu Lys  
 1145 1150 1155  
 Met Pro Ser Leu Leu Ser Glu Ala Phe Cys Asp Asp Leu Glu Arg

1160	1165	1170
Lys Lys Lys Ala Val Ser Phe Phe Asp Asp Val Thr Val Tyr Leu		
1175	1180	1185
Phe Asp Gln Glu Ser Pro Thr Arg Glu Thr Gly Glu Pro Phe Pro		
1190	1195	1200
Ser Thr Lys Glu Ser Leu Pro Thr Phe Leu Glu Gly Gly Pro Ser		
1205	1210	1215
Ser Pro Ser Ala Thr Gly Leu Pro Leu Arg Ala Gly His Ser Pro		
1220	1225	1230
Asp Ser Ser Ala Pro Glu Pro Gly Ser Arg Phe Glu Trp Asp Gly		
1235	1240	1245
Asp Phe Pro Leu Val Pro Gly Lys Ala Ala Leu Val Thr Glu Leu		
1250	1255	1260
Asp Pro Ala Asp Pro Val Leu Ala Ala Pro Pro Thr Pro Ala Ala		
1265	1270	1275
Pro Phe Ser Arg Phe Thr Val Ser Pro Thr Pro Ala Ser Arg Phe		
1280	1285	1290
Ser Ile Thr His Ile Ser Asp Ser Asp Ala Gln Ser Val Gly Gly		
1295	1300	1305
Pro Ala Ala Gly Ala Gly Gly Arg Tyr Thr Glu Ala		
1310	1315	

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